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1  GNTCTAGAAATA GTGGATCCCCC GGGCTGCAGGAA TTCCGACGGCCC CTGAAAGGGCTC TGGTGGGGCTGA
  CNAGATCTTNAT CACCTAGGGGGG CCCGACGTCTTT AAGGCTGCCGGG GACCTTCCCGAG ACCACCCGACT

73  GCGTCTGCTCGC GGGGGCGGGGG ACAGCAGGAAGC AGGTCCGCTGG GCGCTGGGGGCA TCAGTACCGGG
  CGCAGACGGCG CCCCGCGCCCG TGTCTCTCTTCG TCCAGCGCACC CCGACCCCCGT AGTCGATGGCCC

145  GTGGTCCGGGCT GAAGAGCCAGGC AGCCAAGCAGC CACCCCGGGGG TGGCGACTTTG GGGGAGTTGGTG
  CACCAGGCCGA CTCTCTCGGTCCG TCGGTTCCGTCT GTGGGGCCCCC ACCCGCTGAAC CCCTCAACCA

217  CCCCGCCCCCA GGCCTTGGCGGG GTCAATGGGCC CCCCAATCTGGG CCGGGGGCGGTG CGAGTCGGGGCC
  GGGCGGGGGGT CCGGAACCGCC CAGTACCCCGG GGGGTAAAGACC GCCCCCCGCAC GCTCAGCCCGG

1  MetGlyPro ProHisSerGly ProGlyGlyVal ArgValGlyAla

289  CTGCTGCTGCTG GGGGTTTGGGG CTGGTGTCTGGG CTCAGCTTGGG CCTGTCTACTGG AACTCGGCGAAT
  GACCACGACGAC CCCCAAAACCC GACCACAGACC GAGTCGGACCTC GGACAGATGACC TTGAGCGGCTTA

16  LeuLeuLeuLeu GlyValLeuGly LeuValSerGly LeuSerLeuGlu ProValTyrTrp AsnSerAlaAsn

361  AAGAGGTTCCAG GCAGAGGGTGT TATGTGCTGTAC CCTCAGATCGGG GACCGGCTAGAC CTGCTCTGCCCC
  TTCTCCAGGTC CGTCTCCACCA ATACACGACATG GGAFTCTAGCCC CTGGCCGATCTG GACGACCGGG

40  LysArgPheGln AlaGluGlyGly TyrValLeuTyr ProGlnIleGly AspArgLeuAsp LeuLeuCysPro

433  CGGGCCCGGCTT CCTGGCCCTCAC TCCTCTCCTAAT TATGAGTTCTAC AGCTGTACTCTG GTAGGGGGTCT
  GCCCGGCCCGA GGACCGGAGTG AGGAGAGGATTA ATACTCAAGATG TTCCGACATGGAC CATCCCCACGA

64  ArgAlaArgPro ProGlyProHis SerSerProAsn TyrGluPheTyr LysLeuTyrLeu ValGlyGlyAla

505  CAGGGCCGCGC TGTGAGCACCC CCTGCCCAAC CTCTTCTCACT TGTGATCCGCCA GACCTGGATCTC
  GTCCCGGCCCG ACATCCGTGG GGACGGGTTG GAGGAAGATGA ACACTAGCGGT CTGGACCTAGAG

88  GlnGlyArgArg CysGluAlaPro ProAlaProAsn LeuLeuLeuThr CysAspArgPro AspLeuAspLeu

577  CGCTTACCATC AAGTTCACGAG TATAGCCCTAAT CTCTGGGGCCAC GAGTTCCTCTG CACCAGATTAC
  GCGAAGTGGTAG TTCAGTCTCTC ATATCGGGATTA GAGACCCCGTG CTCAGCGCAGC GTGGTCTAATG

112  ArgPheThrIle LysPheGlnGlu TyrSerProAsn LeuTrpGlyHis GluPheArgSer HisHisAspTyr

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FIG. 1A

649 TACATCATTTGCC ACATCGGATGGG ACCGGGAGGGC CTGGAGAGCTG CAGGAGGTTGT TGCCTAACCA
 ATGTAGTAACGG TGTAGCTACCC TGGGCCCTCCG GACTCTCGGAC GTCCCTCCACAC ACGAATGGTCT
 136 TyrlleleAla ThrSerAspGly ThrArgGluGly LeuGlnSerLeu GlnGlyVal CysLeuThrArg
 721 GGCATGAAGGTG CTTCTCCGAGT GGACAAAGTCCC CGAGGAGGGGCT GTCCCCGAAA CCTGTGTCTGAA
 CCGTACTTCCAC GAAGAGGCTCAC CCGTGTTCAGGG GTCTCTCCCGGA CAGGGGCTTTT GGACACAGATT
 160 GlyMetLysVal LeuLeuArgVal GlyGlnSerPro ArgGlyGlyAla ValProArgLys ProValSerGlu
 793 ATGCCCATGGAA AGAGACCAGGAG GCAGCCACAGC CTGGAGCTGGG AAGAGAACTGC CCAGGTACCC
 TACGGGTACCTT TCTCTGGCTCCC CGTCGGGTGTC GACTTCGGACG TTCCTCTTGAC GTTCCACTGGG
 184 MetProMetGlu ArgAspArgGly AlaAlaHisSer LeuGluProGly LysGluHisLeu ProGlyAspPro
 865 ACCAGCAATGCA ACCTCCCGGGGT GCTGAAGCCCC GTCGCCCTTCCC AGCATCCTGCA GTGGCTGGGCA
 TGGTCTGTACCT TGGAGGGCCCCA CGACTTCGGGG GACGGGGAGGG TCGTACGGAGT CACCGACCCGT
 208 ThrSerAsnAla ThrSerArgGly AlaGluGlyPro LeuProProPro SerMetProAla ValAlaGlyAla
 937 GCAGGGGGGCTG GCGTGTCTCTTG CTGGCGTGGCA GGGGCTGGGGT GCCATGTGTGG CGGAGACGGCG
 CGTCCCCCGGAC CGCGACGAGAC GACCCGACCGT CCCCAGCCCCA CGGTACACAAAC GCCTCTGCCGCC
 232 AlaGlyGlyLeu AlaLeuLeuLeu LeuGlyValAla GlyAlaGlyGly AlaMetCysTrp ArgArgArgArg
 1009 GCCAAGCCTTCC GAGATGCCCCAC CCGTGTCTCTGC TCTTTCGGGAGG GGAGGGTCTCTG GGCCTGGGGGT
 CGGTTCGAAGC CTCTCAGCGGTG GACCCAGGACG AGGAAGCCCTCC CCTCCAGAGC CCGACCCCCCA
 256 AlalysProSer GluSerArgHis ProGlyProGly SerPheGlyArg GlyGlySerLeu GlyLeuGlyGly
 1081 GGAGTGGGATG GGACTTCGGAG CTTGAGCCTGGG GAGCTAGGATA GCTCTGGGGGT GCGGGGGCTGCA
 CCTCCACCTTAC CTTGAGCCCTC GACTTCGACCC CTGATCCCTAT CGAGACGCCCA CCGCCCGAGCT
 280 GlyGlyGlyMet GlyProArgGlu AlaGluProGly GluLeuGlyLe AlaLeuArgGly GlyGlyAlaAla
 1153 GATCCCCCTTC TGCCCCCACTAT GAGAAGTGAAT GGTGACTATGG CATCTGTGTAT ATCTGTCAGAT
 CTAGGGGGGAG ACGGGGGTGAAT CTCCTCACTCA CCACTGATACC GTAGGACACATA TAGCACGTCTTA
 304 AspProProPhe CysProHisTyr GluLysValSer GlyAspTyrGly HisProValTyr IleValGlnAsp
 1225 GGGCCCCCCAG AGCCCTCCAAAC ATCTACTACACA TCGATTTCTGTG TTGGAGTGGCCC ATATGCCATACG
 CCGGGGGGGTTC TCGGAGGTTTG TAGATGATGT AGCTAAGACAC AACCTCACCGG TATACTGTATG
 328 GlyProProGln SerProProAsn IleTyrTyrThr SerIleSerVal LeuGluTyrPro IleLeuHisThr

FIG._1B

1297 ATACAACTGTTT TTCAATGCGATCC AAGTGCTCCCGT GTCACTACATTC TTATTTCTCTGT CAAGTTATTACG
 352 TATGTTGACAAA AAGTACGCTAGG TTCACGAGGCA CAGTGATGTAAG AATAAGGCAC GTTCAATAATGC
 IleGlnLeuPhe PheMetArgSer LysCysSerArg ValThrThrPhe LeuPheProVal GlnValIleThr
 1369 ACATGACTTGC CGGATGACTTCA TTATGCTTTACC ACCCTGAACCCA TCCATGCAGGCC TGCAGACACAC
 TGATCTGAACG GCTACTGAAGT AAATCGAATGG TGGGACTTGGT AGCTACGTCCG ACCTCTGCTCTC
 376 ThrSerThrCys ArgMetThrSer PheSerPheThr ThrLeuAsnPro SerMetGlnAla CysArgAlaGln
 1441 ATGGGGGAATC CGAATCAGATGG TGTTCCTGGGG GACAGGATCCTG GGTACGGCTCTG TTTGTGCTTTGTG
 TACCCCTTAAG GCTTAGTCTACC ACAAGAGCCCC CTGTCTAGGAC CCATGCCGAGAC AAACAGAACAC
 400 MetGlyGluPhe ArgIleArgTrp CysPheTrpGly AspArgIleLeu GlyThrAlaLeu PheValLeuVal
 1513 CTTATCTCTTT CTTCGGAGGCTC AATATGCATCAG ACGACACTGCTC GCGCAACGGCG AGTGTGGAGCGG
 GAATAAGAGAA GAACCTCCGAC TTATACGTAGTC TGCTGTGACGAG GCCGTGCCCCG TCACACTCCCG
 424 LeuIleLeuLeu LeuGlyArgLeu AsnMetHisGln ThrThrLeuLeu ArgGlnArgAla SerValGluAla
 1585 GAAGCGGCCAG CATGTCCTCCCTG TGATAGGATTGA AAGAGCTACTGA GAATGGGGGCT TCTCAATGAGAG
 CTTGCGCGGTC GTACGAGGGAC ACTATCTTAAGT TTCTCGATGACT CTATCCCCCGA AGAGTTACTCTC
 448 GluAlaGlyGln HisGlyProLeu
 1657 AGCGAGGCTGC TGTATCATNGGG AACACGGCAGAT CAATCATCCCTG GCAGGTCAGGCA GGAAGTTACTTA
 TCGCTCCGACG ACAATAGTACCC TTGCTCCCTCTA GTTAGTAGGGAC CGTCCAGTCCGT CTTTCAATGAAT
 1729 GCTTCTCTCTCA CTTCTTCTCCAC AGAATTATTAT AGGCTTGTTCCTA AGTTGTAGTGTG TGATCAGATTGC
 CGAAGAGGAAGT GGAAGAAGGGTG TCTTAATAATA TCCGAACAAGGT TCAACATCACAC ACTAGTCTAAGC
 1801 TGCTGCTGTCA GCTCTGTGCTAC CTGGCAGTTCCC CTCATGGAAATC GATATCAAGCTT ATCGATACCGTC
 ACGACGACAGT CGAGACAGATG GACCGTCAAGG GAGTACCTTAAG CTATAGTTCCGA TAGCTATGGCAG
 1873 GACCT
 CTGGA

FIG._1C

FIG._1A

FIG._1B

FIG._1C

FIG._1

1 GNTCTAGAAANTA GTGGATCCCCC GGGCTGCAGAA TTCCAGCGCCC CTGGAAGGCTC TGCTGGGGCTGA
 CNAGATCTTNAT CACCTAGGGGG CCCGACGCTCTT AAGGCTGCCGG GACCTTCCCGAG ACCACCCCGACT
 73 GCGCTCTCCCG GGGGCGCGGGG ACAGCAGGAAG AGGTCCGCGTGG GCGCTGGGGCA TCAGTACCCGG
 CCGAGAGCGG CCCC CGCCCGG TGTCTCTTCG TCCAGCGCAC CCGACCCCGT AGTCGATGGCC
 145 GTGTTCGGGCT GAAGAGCCAGC AGCCAAGCAGC CACCCCGGGGG TGGGCGACTTTG GGGGACTTGGT
 CACCAGGCCCA CTCTCGGCTCG TCGGTTCCGTG GTGGGGCCCCC ACCCGCTGAAC CCCCTCAACCAC
 217 CCCC GCCCCCCA GGCCTTGGCGG GTCATGGGGCC CCCCATTTCTGG CCGGGGGCGTG CGAGTCGGGGC
 GGGCGGGGGT CCGGAACCGCC CAGTACCCCGG GGGGTAAAGACC GGGCCCCGCAC GCTCAGCCCGG
 1 MetGlyPro ProHisSerGly ProGlyGlyVal ArgValGlyVal
 289 CTGTGCTGTG GGGGTTTGGG CTGTGTCTGG CTAGCCCTGG CCGTCTACTTG AACTCGCGCAAT
 GACGACGACGAC CCCC AAAACCC GACCACAGACC GAGTCGGACCTC GGACAGATGACC TTGAGCCGTTA
 16 LeuLeuLeuLeu GlyValLeuGly LeuValSerGly LeuSerLeuGlu ProValTyrTrp AsnSerAlaAsn
 361 AAGAGGTTCCAG GCAGAGGTGT TATGTGTGTAC COTCAGATCGG GACCGGCTAGAC CTGCTCTGCCCC
 TTCTCCAGGTC CGTCTCCACCA ATACACGACATG GGAGTCTAGCCC CTGGCCGATCTG GACGACACGGG
 40 LysArgPheGln AlaGluGlyGly TyrValLeuTyr ProGlnIleGly AspArgLeuAsp LeuLeuCyPro
 433 CGGGCCCGGCT CCTGCCCTCAC TCCTCTCCTAAT TATGAGTTCTAC AAGCTGTACTTG GTAGGGGGTCT
 GCCGGCCCGG GACCGCGAGTG AGGAGAGGATTA ATACTCAAGAT TCGGACATGGAC CATGCCCCAGCA
 64 ArgAlaArgPro ProGlyProHis SerSerProAsn TyrGluPheTyr LysLeuTyrLeu ValGlyGlyAla
 505 CAGGGCCGGCG TGTGAGGACCC CCGCCCCAAC CTCTCTCTCACT TGTGATCGCCA GACCTGGATCTC
 GTCCCGCCCG ACACCTCCGTGG GACGGGGTTG GAGGAAGAGTA ACACTAGCGGT CTGGACCTAGAG
 88 GlnGlyArgArg CysGluAlaPro ProAlaProAsn LeuLeuLeuThr CysAspArgPro AspLeuAspLeu
 577 CGCTTCACCATC AAGTTCAGGAG TATAGCCCTAAT CTCGCGGGCCAC GAGTTCGCTCG CACCACGATTAC
 GCGAAGTGGTAG TTCAAGTCTTC ATATCGGATTA GAGACCCCGGTG CTCGAGGGGAG GTGTGCTGAATG
 112 ArgPheThrIle LysPheGlnGlu TyrSerProAsn LeuTrpGlyHis GluPheArgSer HisHisAspTyr

FIG._2A

649 TACATCATTTGCC ACATCGATTTGG ACCCGGAGGGC CTGGAGAGCGTG CAGGAGAGGTGTG TGCTTAACACAGA
 ATGTAGTAACGG TGTAGCTTACCC TGGGCCCTCCCG GACCTCTCCGAC GTCCCTCCACAC ACGATTTGGTCT
 136 TyrllelleAla ThrSerAspGly ThrArgGluGly LeuGlnSerLeu GinglyGlyVal CysLeuThrArg
 721 GGCATGAAGGTG CTTCTCCGAGTG GGACAAAGTCC CGAGGAGGGGCT GTCCCCCGAAAA CTTGTGTCTGAA
 CCGTACTTCCAC GAAGAGGCTCAC CCTGTTTCAGGG GCTCTCTCCCGA CAGGGGGCTTTT GGACACAGACTT
 160 GlyMetLysVal LeuLeuArgVal GlyGlnSerPro ArgGlyGlyAla ValProArgLys ProValSerGlu
 793 ATGCCCATGGAA AGACACCAGGG GCAGCCCAAGC CTGGAGCGCTGG AAGAGAGACCTG CCAGGTGACCCC
 TACGGGTACCTT TCTCTGGCTCCC CGTCGGGTGCG GACCTCGGACCC TTCTCTCTTGAC GGTCCACTGGG
 184 MetProMetGlu ArgAspArgGly AlaAlaHisSer LeuGluProGly LysGlnAsnLeu ProGlyAspPro
 865 ACCAGCATATGCA ACCTCCCGGGT GCTGAAGGCC CTTGCCCTCTCC AGCATGCTTCCA GTGGCTGGGGCA
 TGGTCTGTACGT TGGAGGGCCCCA CGACTTCGGGG GACGGGGAGGG TCGTACGGAGT CACCGACCCCGT
 208 ThrSerAsnAla ThrSerArgGly AlaGluGlyPro LeuProProPro SerMetProAla ValAlaGlyAla
 937 GCAGGGGGGCTG GCGTGTCTCTTG CTGGCGGTGGCA GGGGTGTTGGGT GCCATGTGTGTG CGGAGACGGCGG
 CGTCCCCCGGAC CGCAGCAGAAAC GACCCGACCGT CCCCAGCCCA CGGTACACAACC GCTCTGCGCGC
 232 AlaGlyGlyLeu AlaLeuLeuLeu LeuGlyValAla GlyAlaGlyGly AlaMetCysTrp ArgArgArgArg
 1009 GCCAAGCCTTTC GAGAGTCGCCAC CTGTCTCTGGC TCCTTCGGGAGG GGAGGGTCTCTG GGCCTGGGGGT
 CGGTTCGAAGC CTCTCAGCGGTG GGACCAAGACG AGGAAGCCCTCC COTCCAGAGAC CGGACCCCGCA
 256 AlalysProSer GluSerArgHis ProGlyProGly SerPheGlyArg GlyGlySerLeu GlyLeuGlyGly
 1081 GGAGGTGGGATG GGACTCTGGAG CTTGAGCCTGGG GAGCTAGGGATA GCTCTGCGGGT GCGGGGGTGC
 CCTCCACCTTAC CTTGAGCCCTC CGACTCGGACCC CTGATCCCTAT CGAGACGCCCA CGGACCCCGCT
 280 GlyGlyGlyMet GlyProArgGlu AlaGluProGly GluLeuGlyIle AlaLeuArgGly GlyGlyAlaAla
 1153 GATCCCCCTTTC TGCCCCCACTAT GAGAAGTGAAT GGTGACTATGG CATCTCTGTGTAT ATCTGTGACGAT
 CTAGGGGGGAG ACGGGGTGATA CTCCTCCACTCA CCATGTATACCC GTAGGACACATA TAGCACGTCTTA
 304 AspProProPhe CysProHisTrp GlyLysValSer HisProValTyr IleValGlnAsp
 1225 GGGCCCCCCCAG AGCCTCCAAAC ATCTACTACAG GTATGAGGGCTC CTCACCGTGGC TATCTGTGATCC
 CCGGGGGGGTTC TCGGAGAGTTTG TAGATGATGTTT CATATCTCCGAG GAGAGTGCACCG ATAGCACTTAGG
 328 GlyProProGln SerProProAsn IleTyrTyrLys ValOP*

FIG._2B

1297 AGCCCTTCTTGG GGTGCTCTCTCCA GTTTAATTCCCTG GTTTCAGGGACA CCTCTAACATCT CGGCCCCCTCTG
 TCGGGAAGAACC CCACAGAGAGGT CAAATTAAAGAC CAAATCTCCTGT GGAGATTGTAGA GCCGGGGGACAC
 1369 GCGCCCAAGCC CTTTACTCTCTCC CGGCTGCTGTCC TCGTCTCCACTT TTAGGATTCTTT AGGATCCCACT
 GGGGGGTCCGG GAAGTGAAGGAG GCCGACGACAG ASCACAGGTGAA AATCCTAAGGA TCCTAAGGTGA
 1441 GCCCCACTTCTT GCCCTCCCGTTT GGCCATGGGTGC CCCCCTCTGTCT CAGTGTCCCTGG ATCCTTTTCTCT
 CGGGGTGAAGA CGGGAAGGCAA CCGGTACCACG CCGGGAGACAGA GTACACAGGACC TAGGAAAAAGGA
 1513 TGGGGAGGGCA CAGGCTCAGCT CTTCTCTGACCA TGACCCAGGCAAT CTTGTCCCTCT CACCACCCAGA
 ACCCTCTCCCT GTCCAGTCCGA GGAGAGACTGTT ACTGGTCCGTA GGAACAGGGGA GTGGGTGGTCT
 1585 GCTAGGGGGG AACAGCCACCT TTTGGTGGCAC GCCTTCTTCTT GCCTCTCACTGG TTTTCTCTTCTC
 CGATCCCGCCC TTGTCCGTGGA AAACAACCTG CGGGAAGAAGA CGGAGAGTGACC AAAAGAGAAG
 1657 TATCTCTATTTC TTTCCTCTCTT CCGTCTTAGGT CTGTTCTTCTTC CCTAGCATCTC CTCCCACATCT
 ATAGAGATAAG AAAGGAGAGAA GGCAGAGATCCA GACAAGAAGA GGCATCTAGAG GAGGCTGTAGA
 1729 CCTTTCACCTC TTGGTCTTATT CTTGTGCTCTC CCATCTCTGGG TGGGGGCATCAA AGCATTTCTCCC
 GGAAGTGGGAG AACGAGAATA GGACACGGAG GGTAGAGACC ACCCCGTAGTT TCGTAAGAGG
 1801 CTTAGCTTTTCA GCGCTCTCTGA CCTCTATACCA ACCACTCCCTC AGTCTGCCAAA ATGGGGGCCCTTA
 GAATCGAAATC GGGGGGAAGCT GGAGATATGTT TGGTGAAGGAG TCAGACGGTTTT TACCCCGGAAT
 1873 TGGGGAAGGCTC TGACACTCCACC CCAGCTAGGCC ATGGGCACCCAG GCTCCATTCTT GGCTCGGGCCAG
 ACCCTTCCGAG ACTGTGAGTGG GTTCGATCCCG TACCCTGTCTCC CGAGGTAGAGA CGGACCGGTC
 1945 GCCTCTACATAC TTACTCCAGCA TTGTGGGTGGTT GGGTCATGACAG CTACCATGAGAA GAAGTCTCCGT
 CGGAGATGTATG AATGAGTCCGT AAACCCACCA CCCATCTGTCT GATGTACTCTT CTTACAGGGCA
 2017 TTTCTCCAGTGG CCAATAGCAAG TATGAACGGTC GGGACATGTAT GACTTGGTCTGA TCGTGAATGGC
 AAACAGTCCAC GGTATCTGTTT ATACTTGGCCAG CCTCTACATAC CTGAACCAACT ACGACTTACCCG

FIG._2C

2089 CACTTGGGACCG GAAGTGACTTGC TCCAGACAAGAG GTGACCAGGCC CCTGACGAAATGG CCTGGGAAGTAG
 GTGAACCCCTGGC CTTCACTGAACG AGGTCTGTCTC CACTGTCTTACC CTTGTCTTACC GGACCCCTCATC
 2161 CAGAAGCAGTGC AGCAGAACTGG AAGTGCCTTCAT CCAGGACAGGAA GTAGCACTTCTG AARACAGGAAGTG
 GTCTTTCGTACG TCGTCCCTTGACC TTCAAGGAAGTA GGTCTGTCTCTT CATCGTGAAGAC TTTGTCTCTTCA
 2233 GTCTGGCTGGAA CTCCAAGTGGCT TAGTCTGGGGA TCAGGAGGTGGG AGGTGATGGTT CTTATTCGTGGG
 CAGACCGACCTT GAGGTTCACCG ATCAGACCCCT AGTCTCCACCC TCACCTACCAA GAATAAGACAC
 2305 AGAAGAAGGCG GGAAGAACTCC TTTCAAGGAGGAA GCTGGAACCTTAC TGACTGTAAAG GTTAGAGGTGGA
 TCTTCTTCCCGC CCTTCTTGAAG AAGTCTCTCTT CGACCTTGAATG ACTGACATTCTC CAATCTCCACCT
 2377 CCGA
 GGCT

FIG..2D

FIG..2A

FIG..2B

FIG..2C

FIG..2D

FIG..2

AL-2b.L	1	GN	CT	AG	AA	NT	AG	TG	GA	TCCC	CC	CG	GG	CT	GC	AG	GA	AT	CC	GA	CG	CC	CC	CT	
AL-2b.L	51	GA	AG	GC	CT	CT	GT	GG	GC	TG	AG	CG	CT	CT	GC	CG	GG	GC	CG	GG	CG	CG	CG	CG	
AL-2b.L	101	CA	GA	AG	CA	AG	TC	CG	CG	TG	GG	CG	CT	GT	GG	GG	CA	TC	AG	CT	AC	CG	GG	TG	
AL-2b.L	151	CG	GC	CT	GA	AG	CA	AG	CA	GC	CA	AG	CA	GC	CA	CC	CG	GG	GG	GT	GG	GC	CG	CA	
AL-2b.L	201	TT	GG	GG	GA	GT	GG	TG	CC	CC	CG	CC	CA	AG	CC	TT	GG	CG	GG	GT	CA	TG	GG	GC	
AL-2b.L	251	CC	CC	CA	AT	CT	GG	GC	CG	GG	GC	TG	CG	AG	TC	GG	GG	CC	CT	GC	TG	CT	GT	CT	
AL-2b.L	301	GG	GG	TT	TT	GG	GG	CT	GG	TG	CT	GG	GC	TC	AG	CC	TG	GA	CC	CT	GT	CT	ACT	GGAA	
AL-2b.L	351	CT	CG	GC	GA	ATA	AG	AG	TT	CC	AG	GC	AG	AG	GG	TG	GG	TT	AT	TG	TG	CT	GT	AC	
AL-2b.L	401	AG	AT	CG	GG	GA	CC	GG	CT	AG	AC	CT	GT	CT	GG	CC	CG	GG	CC	GG	CC	CT	CT	GGC	
AL-2b.L	451	CC	TC	ACT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	CT	
AL-2b.L	501	TG	CT	CT	AG	GG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	
H10006	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
AL-2b.L	551	CT	GT	GA	TC	GC	CC	CA	GA	CC	TG	GA	TC	CT	CG	CT	TC	CA	CC	AT	CA	AG	TT	CC	AG
H10006	43	CT	GT	GA	TC	GC	CC	CA	GA	CC	TG	GA	TC	CT	CG	CT	TC	CA	CC	AT	CA	AG	TT	CC	AG
AL-2b.L	601	TA	TA	GC	CC	TA	AT	CT	CG	GG	CC	CA	CG	AG	TT	CC	GC	TC	GC	CA	CC	AG	TT	ACT	TA
H10006	93	TA	TA	GC	CC	TA	AT	CT	CG	GG	CC	CA	CG	AG	TT	CC	GC	TC	GC	CA	CC	AG	TT	ACT	TA
AL-2b.L	651	CA	TC	ATT	GC	CA	CA	TC	CG	GA	TG	GG	AC	CC	CG	GG	AG	GG	CT	GG	AG	GC	CT	TC	CA
H10006	143	CA	TC	ATT	GC	CA	CA	TC	CG	GA	TG	GG	AC	CC	CG	GG	AG	GG	CT	GG	AG	GC	CT	TC	CA
AL-2b.L	701	GA	GT	GT	GT	GC	CT	TA	AC	CA	AG	GC	CA	TG	AA	GG	TG	CT	TC	CG	AG	TT	GG	AC	AA
H10006	193	GA	GT	GT	GT	GC	CT	TA	AC	CA	AG	GC	CA	TG	AA	GG	TG	CT	TC	CG	AG	TT	GG	AC	AA

FIG._3A

AL-2b.L 751 A G T C C C G A G G A G G G G C T G T C C C C C G A A A A C C T G T G T C T G A A A T G C C C A T
 H1006 243 A G T - C C C G A G G A G G G G C T G T C C C C C G A A A C C T G T G T C T G A A A T G C C C A T
 AL-2b.L 801 G G A A G A G A C C G A G G G C A G C C C A C A G C C T - G G A G C C T - G G G A A G G A G A A
 H1006 292 G G A A G A G A C C G A G G G C A G C C C A C A G C C T G G A G C C T G G G G A A G G A G A A
 AL-2b.L 849 C C T G C C A G G T G A C C C C A C C A G C A A T G C A A C C T C C C G G G T - - G C T G A A G G
 H1006 342 C C T G C C A G G T G A C C C C A C C A G C A A T N C A A C C T C C G G G T G C T T G A A G G
 AL-2b.L 897 C C C C T - - G C C C C T C C C A G C A - T G C C T G C A G T - - G G C T G G G C A G C A G G
 H1006 392 G C C C T T G A C C C T T T C C C A G C A T T G C N T T G C A N T T G G T T N G G G C A G C A N G
 AL-2b.L 942 G G G C C - - - T G G C G C T G C T T G C T G G C G T G G C A G G G C T G G G G G T G C C
 H1006 442 G G G G N G T T T G G C
 AL-2b.L 988 A T G T G T G G C G G A G A C G C G G G C C A A G C C T C G G A G A G T C G C C A C C C T G G
 AL-2b.L 1038 T C C T G G C T C T T C G G A G G G A G G G T C T C T G G C C T G G G G G T G A G G T G
 AL-2b.L 1088 G A T G G A C C T C G G A G G C T G A G C C T G G G G A G C T A G G G A T A G C T C T G C G G
 AL-2b.L 1138 G T G G C G G G C T G C A G A T C C C C C C T C T G C C C C A C T A T G A G A A G G T G A G
 AL-2b.L 1188 T G G T G A C T A T G G G C A T C C T G T G T A T A T C G T G C A G G A T G G G C C C C C A G A
 AL-2b.L 1238 G C C C T C A A C A T C T A C A C A T C G A T T T C T G T G T T G G A G T G G C C C A T A
 AL-2b.L 1288 T T G C A T A C G A T A C A A C T G T T T T T C A T G C G A T C C A A G T G C T C C C G T G T C A C

AL-2b.L 1338 T A C A T T C T T A T T C C T G T G C A A G T T A T T A C G A C A T C G A C T T G C C G G A T G A
AL-2b.L 1388 C T T C A T T A G C T T T A C G A C C C T G A A C C C A T C C A T G C A G G C C T G C A G A G C A
AL-2b.L 1438 C A G A T G G G G G A A T T C C G A A T C A G A T G G T G T T T C T G G G G G G A C A G G A T C C T
AL-2b.L 1488 G G G T A C G G C T C T G T T G T G C T T G T G C T T A T T C T T C T T C T T G G G A G G C T G A
AL-2b.L 1538 A T A T G C A T C A G A C G A C A G T G C T C C G G C A A C G G G C C A G T G G A G G C G G A A
AL-2b.L 1588 G C C G G C C A G C A T G G T C C G C T G T G A T A G G A T T G A A A G A G C T A C T G A G A A T A
AL-2b.L 1638 G G G G G C T T C T C A A T G A G A G A G C G G A G G C T G C T G T T A T C A T G G G A A C C A G G
AL-2b.L 1688 C A G A T C A A T C A T C C C T G G C A G G T C A G G C A G A A G T T A C T T A G C T T C T C C T
AL-2b.L 1738 T C A C C T T C T C C C A C A G A A T T T A T T A T A G G C T T G T T C C A A G T T G T A G T G T
AL-2b.L 1788 G T G A T C A G A T T C G T G C T G C C T G T C A G C T C T G T G C T A C C T G G C A G T T C C C C
AL-2b.L 1838 T C A T G G A A T T C G A T A T C A A G C T T A T C G A T A C C G T C G A C C T

FIG._3C

FIG..3A

FIG..3B

FIG._3

FIG...3C

lerk2	1	MA	RP	IG	QR	WL	GK	WL	LV	AM	VV	WA	LC	RL	AT	PL	AK	KN	LE	PV	SW	SL	NP	KFL	SG	GK	G																							
huHTKL	1	MA	VR	RD	SV	WK	YC	WG	VL	ML	VL	VL	LC	RL	AT	PL	AK	KN	LE	PV	WN	SS	NP	KFL	PG	Q	G																							
AL2.sht	1	MG	PP	HS	GG	VR	VG	AL	LL	GV	LV	SL	LC	RL	AT	PL	AK	KN	LE	PV	WN	SA	NK	RF	QA	EGG																								
AL2.long	1	MG	PP	HS	GG	VR	VG	AL	LL	GV	LV	SL	LC	RL	AT	PL	AK	KN	LE	PV	WN	SA	NK	RF	QA	EGG																								
lerk2	50	LV	Y	P	K	I	G	D	K	L	D	I	C	P	R	A	---	E	A	G	R	---	P	Y	E	Y	K	L	Y	L	V	R	P	E	Q	A	A	C	S	T	V	L	D							
huHTKL	48	LV	Y	P	Q	I	G	D	K	L	D	I	C	P	K	V	---	D	S	K	T	V	G	Q	Y	E	Y	K	V	Y	M	V	D	K	D	Q	A	D	R	C	T	I	K	E						
AL2.sht	48	YV	L	P	Q	I	G	D	R	L	D	L	C	P	R	A	R	P	P	G	P	H	S	S	P	N	Y	E	F	Y	K	L	Y	L	V	G	A	Q	G	R	R	C	E	A	P	P	A			
AL2.long	48	YV	L	P	Q	I	G	D	R	L	D	L	C	P	R	A	R	P	P	G	P	H	S	S	P	N	Y	E	F	Y	K	L	Y	L	V	G	A	Q	G	R	R	C	E	A	P	P	A			
lerk2	95	P	N	V	L	V	T	C	N	R	P	E	Q	E	I	R	F	T	I	K	F	Q	E	F	S	P	N	Y	M	G	L	E	F	K	K	H	D	Y	I	T	S	T	S	N	G	S	L	E	G	
huHTKL	95	N	T	P	L	L	N	C	A	K	P	D	Q	D	I	K	F	T	I	K	F	Q	E	F	S	P	N	Y	M	G	L	E	F	K	K	H	D	Y	I	T	S	T	S	N	G	S	L	E	G	
AL2.sht	98	P	N	L	L	T	C	D	R	P	D	L	R	F	T	I	K	F	Q	E	S	P	N	L	W	G	H	E	F	R	S	H	D	Y	I	A	T	S	D	G	T	R	E	G						
AL2.long	98	P	N	L	L	T	C	D	R	P	D	L	R	F	T	I	K	F	Q	E	S	P	N	L	W	G	H	E	F	R	S	H	D	Y	I	A	T	S	D	G	T	R	E	G						
lerk2	145	L	E	N	R	E	G	G	V	C	R	T	R	A	M	K	I	L	M	K	V	G	Q	D	P	N	A	V	T	P	E	Q	L	T	S	R	P	S	K	E	A	D	N	T	V	K	M	A	T	Q
huHTKL	145	L	D	N	Q	E	G	G	V	C	Q	T	R	A	M	K	I	L	M	K	V	G	Q	D	P	N	A	V	T	P	E	Q	L	T	S	R	P	S	K	E	A	D	N	T	V	K	M	A	T	Q
AL2.sht	148	L	E	S	L	Q	G	G	V	C	L	T	R	G	M	K	V	L	L	R	V	G	S	P	R	G	G	A	V	P	R	K	P	V	S	E	M	P	M	E	R	D	R	G	A	A	H	S	L	
AL2.long	148	L	E	S	L	Q	G	G	V	C	L	T	R	G	M	K	V	L	L	R	V	G	S	P	R	G	G	A	V	P	R	K	P	V	S	E	M	P	M	E	R	D	R	G	A	A	H	S	L	

FIG._4A

lexk2	195	A P G S R G S L G D S D G K H E T V N Q E E K S G P G A S G G S S G D P D G F F N S K V A L F A I A V
huITKL	189	T N G - R S T T S P I F V K P N P G S S T D G N S A G H S G - - - - - N N I L G S E V A L F A G I
AL2.sht	198	- P G K E N L P G D P T S N A T S R G A E G P L P P P S M P A V A G A A G G L - - - A L L L L G V A
AL2.long	198	- P G K E N L P G D P T S N A T S R G A E G P L P P P S M P A V A G A A G G L - A L L L L G V A

	245	232	244	244
lerk2	G A G C V	I F L L I I F L T	V L L L K L R	R R R K H T Q - Q R A A A L S L S T L A S
huHTKL	A S G C I	I F I V I I T V L V L L K Y R R	R R R K H S P - Q H T T T L S L S T L A T	P K R S G N
AI2.sht	G A G G A	- - - - M C W R R R R A K P S E S R H P G P G S F G R G G S L G L G G - - -	G G G M G	
AI2.long	G A G G A	- - - - M C W R R R R A K P S E S R H P G P G S F G R G G S L G L G G - - -	G G G M G	

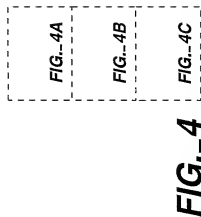
lerk2	294	T	A	G	T	E	P	S	D	I	I	P	L	R	-	-	-	T	T	E	N	N	Y	C	P	H	Y	E	K	V	S	G	D	Y	G	H	P	V	I	V	Q	E	M	P	P	Q	S	P
huHTKL	281	N	N	G	S	E	P	S	D	I	I	P	L	R	-	-	-	T	A	D	S	V	F	C	P	H	Y	E	K	V	S	G	D	Y	G	H	P	V	I	V	Q	E	M	P	P	Q	S	P
AL2L2.sht	285	P	R	E	A	E	P	G	E	L	G	I	A	L	R	G	G	A	A	D	P	P	F	C	P	H	Y	E	K	V	S	G	D	Y	G	H	P	V	I	V	Q	D	G	P	P	Q	S	P
AL2L2.long	285	P	R	E	A	E	P	G	E	L	G	I	A	L	R	G	G	A	A	D	P	P	F	C	P	H	Y	E	K	V	S	G	D	Y	G	H	P	V	I	V	Q	D	G	P	P	Q	S	P

[illegible]

FIG. 4B

	345	332	339	385	435
lexk2	-	-	-	-	-
huTKL	-	-	-	-	-
AL2.sht	-	-	-	-	-
AL2.long	S F T T L N P S M Q A C R A Q M G E F R I R W C F W G D R I L G T A L F V L V L I L L G R L N M H	K V	K V	K V	K V
AL2.long	Q T T L L R Q R A S V E A E A G Q H G P L				

FIG. 4C



1 MA-RPGQRWLSKWLVA MVVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKG
1 MAVRDSVWKYCWGLVMV--LCRTAISKSVLEPIYWNSSNSKFLPGQG
1 MGPPHSGP-GGVRVGA L L L--LGVLG L V SGLSLEPVYWNSSANKRFQAE EG

50 LVIYPKIGDKLDIICPRA- - - EAGR- - - PVEYYKLYLV RPEQAACSTVLD
LERK2
48 LVLYPQIGDKLDIICPKV- - - DSKTVGQVEYYKLYLVMDKDAQDRCTIKKE
huTKL
48 YVLYPQIGDRLLDLCPRARPPGPHSSPNVEFLYKLYLVGGAQGRRC EAPPA
AL2.long

LERK2 95 PNV LVTCNKPHQEIRFTIKFQEFSPNYMGLFEEKKYHDDYITSTSNGLSLEG
 huHTKL 95 NTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKKNKDYIISTSNGLSLEG
 AL2.long 98 PNL L L T C D R P D L D L R F T I K F Q E Y S P N L W G H E F R S H H D Y I I A T S D G T R E G

LERK2 145 L E N R E G G V C R T R T M K I V M K V G Q D P N A V T P E Q L T T S R P S K E S D N T V K T A T Q
 huTKL 145 L D N Q E G G V C Q T R A M K I L M K V G Q D A S S - - - - A G S T R N K D P T R R P E L E A G
 AL2.long 148 L E I S L Q G G V C L T R G M K V L L R V G Q S P R G - - - - G A V P R K P V S E M P M E R D R G

195 LERK2 A P G R G S Q G D S D G K H E T V N Q E E K S G P G A G G G S G D S D S F F N S K V A L F A A V G
 huHTKL 189 T N G R S S I T S P F V K P N P G S S T D G N S A G H S G - - - - N N I L G S E V A L F A G I A
 AL2.long 192 A A H S L E P G K E N L P G D P T S N A T S R G A E - - - - - G P L P P S M P A V A G A A

FIG. 5A

LERK2 245 AGCV I F L L I I I F L T V L L K L R K R R K H T Q R A A L S L . . . S T L A S P K G G S
 huHTKL 233 S G C I I F I V I I I T L V L L K Y R R R R K H S P Q H T T L S L . . . S T L A T P K R S G
 AL2_long 233 G G L A L L L G V A G A G G A C M C W R R R R A K P S E S R H P G P G S F G R G G S L G L G G G G G

292 - **G**T A G T E P S D I I P L R - - - T T E N N Y C P H Y E K V S G D Y G H P V Y I V Q E M P P Q S
LERK2
280 - N N N G S E P S D I I P L R - - - T A D S V F C P H Y E K V S G D Y G H P V Y I V Q E M P P Q S
huHTKL
283 M G P R E A E P G E L G I A L R G G G A D P P F C P H Y E K V S G D Y G H P V Y I V Q D G P P Q S
AL2.long

LERK2 338 P A N I Y Y - - - - -
 huHTKL 326 P A N I Y Y - - - - -
 A12.L long 333 P N I Y Y T S I S V L E W P I L H T I Q L F F M R S K C S R V T T F L F P V Q V I T T S T C R M T

LRRK2 344 K V
 huHTKL 332 K V
 AL2.Long 383 S F S F T T L N P S M Q A C R A Q M G E F R I R W C F W G D R I L G T A L F V L V L I L L G R L N

AL2.long 433 MHQTTLRQRASVEAEAGQHGPL

FIG. 5B

FIG. 5A

FIG. 5B

FIG. 5